SEQUENCE LISTING

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<110> Korman, Alagara
Halk, Edward L.
Lonberg, Nils
Medarex, Inc.

<120> Human CTLA-4 Antibodies and Their Uses

<130> 014643-010510US

<140> US 09/644,668 <141> 2000-08-24

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<160> 41

<170> PatentIn Ver. 2.1

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Bw

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ggtgacattt atatcatatg atggaaacaa taaatactac gcagactccg tgaagggccg 180
attcaccatc tccagagaca attccaagaa cacgctgtat ctgcaaatga acagcctgag 240
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tcctcatcta tggtgcattc agcaggcca ctggcatccc agacaggttc agtggcagtg 180
ggtctgggac agacttcact ctcaccatca gcagactgga gcctgaagat tttgcagtgt 240
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321

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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcacc
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<212> PRT
<213> Homo sapiens
<223> light chain variable region predicted sequence for
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Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser
<210> 6
<211> 325
<212> DNA
<213> Homo sapiens
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<223> light chain variable region (Vk), 10D1 from Vk
      A-27
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cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300
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<212> PRT <213> Homo sapiens <220> <223> light chain variagle region predicted sequence for 10D1 from Vk A-27 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly 10 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser 25 20 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 <210> 8 <211> 325

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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
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caagggacca aggtggaaat caaac

<210> 9
<211> 108
<212> PRT
<213> Homo sapiens
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<223> light chain variable region predicted sequence for

4B6 from Vk A-27

<400> 9

<212> DNA

<213> Homo sapiens

<210> 7 <211> 108

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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr 85 90

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<211> 322

<212> DNA

<213> Homo sapiens

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<210> 13

<211> 107

<212> PRT

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<223> light chain variable region predicted sequence for 1E2 from Vk L-15

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly 50 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro 65 70 75 80

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gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
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<213> Homo sapiens
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<223> heavy chain variable region predicted sequence for
      VH 3-30.3 germline
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
                                 25
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

Ala Arg

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
                                 25
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
                             40
Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
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Leu Val Thr Val Ser Ser
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<213> Homo sapiens
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<210> 19
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<213> Homo sapiens

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<223> heavy chain variable region predicted sequence for 4B6 from VH 3-30.3

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300

10

1

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly Ser Asn Lys His Tyr Ala Asp Ser Val 55 . Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser 115 <210> 20 <211> 296 <212> DNA <213> Homo sapiens <220> <223> VH 3-33 germline sequence <400> 20 caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60 teetgtgeag egtetggatt eacetteagt agetatggea tgeactgggt eegeeagget 120 ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaagtaa taaatactat 180 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240 ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagaga <210> 21 <211> 98 <212> PRT <213> Homo sapiens <220> <223> heavy chain variable region predicted sequence for VH 3-33 germline <400> 21 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 40 Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 55

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg

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<223> heavy chain variable region VH 1E2 from VH 3-33

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Phe Tyr Cys
85 90 95

Ala Arg Ala Pro Asn Tyr Ile Gly Ala Phe Asp Val Trp Gly Gln Gly

Thr Met Val Thr Val Ser Ser 115

Bro

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<213> Homo sapiens
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<223> light chain CDR1 (HuMab 4B6)
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<211> 11
<212> PRT
<213> Homo sapiens
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                5
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<223> heavy chain CDR1 (HuMab 1E2)
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 Gly Ala Ser Ser Arg Ala Thr
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 <400> 32
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 Gly
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Phe Ile Ser Tyr Asp Gly Ser Asn Lys His Tyr Ala Asp Ser Val Lys
Gly
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Gly
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<211> 9
<212> PRT
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bro

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<223> heavy chain CDR3 (HuMab 10D1, 4B6)
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<213> Artificial Sequence
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